

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: November 29, 2001, 04:05:59 ; Search time 10554.9 Seconds

(without alignments)
1800.570 Million cell updates/sec

Title: US-09-526-329-38

Perfect score: 1152
1 gagcgaggtccggtgtcag.....aaaaaaaaaaaaaaaa 1152

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:*

1: gb_ha:*

2: gb_hg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_om:*

20: em_ov:*

21: em_ov:*

22: em_pat:*

23: em_ph:*

24: em_pl:*

25: em_ro:*

26: em_sts:*

27: em_sy:*

28: em_un:*

29: em_vl:*

30: em_hgtg_hum:*

31: em_hgtg_inv:*

32: em_hgtg_rod:*

33: em_hgtg_hum:*

34: em_hgtg_inv:*

35: em_hgtg_rod:*

36: em_hgtg_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1152	100.0	1152	9	AF110466	AF110466 Homo sapi
2	1150.4	99.9	1177	9	AF137027	AF137027 Homo sapi
3	963	83.6	3144	9	AB035343	AB035343 Homo sapi
4	963	83.6	3240	9	AB035342	AB035342 Homo sapi
5	963	83.6	3532	9	AB035340	AB035340 Homo sapi
6	963	83.6	3599	9	AB035341	AB035341 Homo sapi
7	718	62.3	11438	2	AC010356	AC010356 Homo sapi
8	718	62.3	20484	2	AC010359	AC010359 Homo sapi
9	701.6	60.9	137808	2	AC008889	AC008889 Homo sapi
10	701.2	60.9	6466	9	AF110465	AF110465 Homo sapi
11	700.4	60.8	1248	9	AF110467	AF110467 Homo sapi
12	699.6	60.7	16308	9	CNS01DX2	AL139020 Human chr
13	699.6	60.7	210791	9	CNS01DX7	AL133467 Human chr
14	695.4	60.4	110879	9	AC016603	AC016603 Homo sapi
15	687.6	59.7	1717	9	AB02527283	AB025272 Homo sapi
16	687.2	59.7	1722	9	AB018563	AB018563 Homo sapi
17	189	16.4	627	9	AB02527281	AB025272 Homo sapi
18	169.4	14.7	753	9	AB02527282	AB025272 Homo sapi
19	64.4	5.6	7218	6	I6484	I6484 Sequence 14
20	63	5.5	1040	10	AF195492	AF195492 Mus muscu
21	62.8	5.5	1231	9	BC003574	BC003574 Homo sapi
22	62.8	5.5	1240	9	BC005831	BC005831 Homo sapi
23	62.8	5.5	1324	6	AR086519	AR086519 Sequence
24	62.8	5.5	1324	6	HSTC1	X82240 H.sapiens m
25	56.6	4.9	1048	10	AF195493	AF195493 Mus muscu
26	55	4.8	1020	10	AF195489	AF195489 Mus muscu
27	51.2	4.4	1058	10	AF195490	AF195490 Mus muscu
28	51	4.4	16308	9	CNS01DX2	AL139020 Human chr
29	50	4.3	4922	6	AR086521	AR086521 Sequence
30	48	4.2	1338	10	AF031956	AF031956 Mus muscu
31	48	4.2	1338	10	NMRNATC1	Y15376 Mus muscu
32	47.4	4.1	957	10	AF195491	AF195491 Mus muscu
33	45.6	4.0	10732	6	E32986	E32986 Gene encodi
34	44.2	3.8	124499	2	AC007307	AC007307 Mus muscu
35	42.6	3.7	134148	2	AL358512	AL358512 Homo sapi
36	42	3.6	1040	10	AF195488	AF195488 Mus muscu
37	41.6	3.6	1719	6	AX127641	AX127641 Sequence
38	41.2	3.6	1770	5	CCP2A	Z72491 C. carpio mr
39	41	3.6	1555	9	BC001141	BC001141 Homo sapi
40	41	3.6	1555	9	BC008033	BC008033 Homo sapi
41	40.8	3.5	89723	9	AP001417	AP001417 Homo sapi
42	40.8	3.5	100000	9	AP000018	AP000018 Homo sapi
43	40.8	3.5	100000	9	AP000160	AP000160 Homo sapi
44	40.8	3.5	340000	9	AP001730	AP001730 Homo sapi
45	40.4	3.5	179463	2	AL596453	AL596453 Homo sapi

ALIGNMENTS

RESULT 1

AF110466 1152 bp mRNA 18-MAR-1999

DEFINITION Homo sapiens T-cell leukemia/lymphoma 1B (TCL1B) mRNA, complete cds.

ACCESSION AF110466

VERSION AF110466.1 GI:4324704

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1152)

AUTHORS Pekarisky,Y., Hallas,C., Isobe,M., Russo,G. and Croce,C.M.

TITLE Abnormalities at 14q32.1 in T cell malignancies involve two oncogenes

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (6), 2949-2951 (1999)

MEDLINE 99178995

REFERENCE 2 (bases 1 to 1152)

AUTHORS Pekarisky,Y., Hallas,C. and Croce,C.M.

TITLE Direct Submission
JOURNAL Submitted (02-DEC-1998) KCI, Thomas Jefferson University, 233 South
10th Str. BLSB 1033, Philadelphia, PA 19107, USA
FEATURES Location/Qualifiers
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1. 1152
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="14"
/map="14q32.1"
1. 1152
/gene="TCL1B"
28. 414
/gene="TCL1B"
/codon_start=1
/product="T-cell leukemia/lymphoma 1B"
/protein_id="ABD1697.1"
/db_xref="GI:4324705"
/translation="MASEASVRLGVPPGLMIDRPGIYEDSGRTWTVVFNPSR
EMARASQSRYSPTVHLMOMAVHTRRLSSGOMFSPQIPAVWOLYGRKRYRAADS
FWEIADHGQIDSMEDLVITYQPERKD"
BASE COUNT 232 a 325 c 324 g 271 t
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Matches 1152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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61 CCCCTGAGCGTCTGTGGTATCCAGAGCCTGTGCATCTACGAAGATGAGAGGGAGAAAC 120
121 tgggtgactgt 180
121 TGGGTGACTGT 180
181 tgggtgactgt 240
181 TGGGTGACTGT 240
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241 GAGCTACTCTCCCTCCGAGCAGATGCCCTCTCCAGCTGCCGCCGCGTGGAGACTTAC 300
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361 attgactcatalgagcagctgtgtcctaataatacagccgagagagaagactgacttg 420
361 ATTGACTCATATGAGCAGCTGTGTCTTACATATACGCGAGAGAAACTGACTGCG 420
421 gaatgctgagcctctgtgagcctctctctctgagcctgtgtctctctctctctctcag 480
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481 tggagatctctatgtactgtctctctctctctctctctctctctctctctctctct 540
481 TGGAGATCTCTATGTACTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 540
541 gaagcagatgagagccctctgacacatgcttctctctctctctctctctctctctct 600
541 GAAGCAGATGAGAGCCCTCTGACACATGCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 600
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601 CCTGTCCCAACTCAAGCTCTGTAACCTTAGAGCAGCCTGTGAGCTGACTGAGCCTCT 660
661 gtctgtgctgagcagcttccctctgtgctgagcagctgtggtgtctctctctctctgt 720

Db 661 GTCTGTCTGAGCAGATTTCCTCCCTGCTGAGCTGAGCTGTGAGCTTCTCTCTCTGT 720
Qy 721 gccctcactgctgact 780
Db 721 GCCCTCAGTGTGATCTTCTAGATGCACTCCCAATCCCTTCAATGCCACAGAGTGT 780
Qy 781 gtgccagcagagcctccagacccccagctgagctctgtgattggaactcacatctggc 840
Db 781 GTGCCAGCAGAGCCTCCACACACCCAGTGCAGCTGTGATGGAAGAACTCACATGCGC 840
Qy 841 aggcagctgtctgtcttaagagatgcatctagagagagccagctgtgattgagcttg 900
Db 841 AGGCAGCTGTCTGTCTTAAGAGATGCACTTAGAGAGAGCCAGCTGTGATGAGCTTG 900
Qy 901 atgcccctgtggtatctagctctgtctgtaacacttggccgaaatagatccagctgagca 960
Db 901 ATGCCCTGTGGGTATCAGTTCTGTGACACTTGGCCCGAATATGATCAGTCTGAGCA 960
Qy 961 agcaatgtacacccgagcctcagctgagccatctctcagctgtgagagatgagagatg 1020
Db 961 AGCAATGTACACCCGAGCCTCAGTACGCCATCTGCACAGTGGGAGCATGAGAGATGG 1020
Qy 1021 gtttgctgtgtctctgtcttacttcaagctcctcagctcagagagagagctgctgctg 1080
Db 1021 GTTTGCTGTGTCTCTGTCTTACTTCAAGTCTTCAAGCTCAGGAGAGGATGCTAGTCTG 1080
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Db 1081 AAGTGACCTCAACAGTGTGTAAATTAACCTTATTGCTCACTGTCAAAAAA 1140
Qy 1141 aaaaaa 1152
Db 1141 AAAAAA 1152

RESULT 2
AF137027 1177 bp mRNA PRI 13-MAY-1999
LOCUS Homo sapiens syncytiotrophoblast-specific protein mRNA, complete
DEFINITION cds
ACCESSION AF137027
VERSION AF137027.1 GI:4809182
KEYWORDS
SOURCE
ORGANISM human.
human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Jiang, B. and Mendelson, C.R.
TITLE A syncytiotrophoblast-specific gene Syn-1 cloned from human
syncytiotrophoblast substracted cDNA library
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1177)
AUTHORS Jiang, B. and Mendelson, C.R.
TITLE Direct Submission
JOURNAL Submitted (24-MAR-1999) Biochemistry, UT Southwestern Medical
Center at Dallas, 5323 Harry Hines Blvd., Dallas, Texas 75235, USA
FEATURES Location/Qualifiers
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1. 1177
/organism="Homo sapiens"
/db_xref="taxon:9606"
47. 433
/note="Syn-1 protein"
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/db_xref="GI:4809183"
/translation="MASEASVRLGVPPGLMIDRPGIYEDSGRTWTVVFNPSR
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FWEIADHGQIDSMEDLVITYQPERKD"
BASE COUNT 242 a 328 c 332 g 275 t
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Query Match 99.9%; Score 1150.4; DB 9; Length 1177;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1151; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 61 cccctcgccgtctgtgattccagagccttgcatcactcaagaatagaggggaggaacc 120
DB 80 CCCCCTGCGCGCTGTGTGATTCAGAGAGCCTGCGCATCTACGAATAGAGAGGAGGAGAAC 139
QY 121 ttggtactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 180
DB 140 TGGGTACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 199
QY 181 ggcagagatatgaaccagcatcagtgacactgtgtgtgtgtgtgtgtgtgtgtgtgtgt 240
DB 200 GCGAGGAGATGATGAAACCCAGATACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 259
QY 241 gacgtactctctcccgccagatgtcccttcctccagctgcccgctgtgtgtgtgtgt 300
DB 260 GAGCTACTCTCTCCGCGCCAGATGCTCTTCTCCAGCTGCCCGCGTGTGTGTGTGTGTGT 319
QY 301 cccggagagaaataccagagcagcgaattccagtttctgtgtgtgtgtgtgtgtgtgtgt 360
DB 320 CCGGAGGAGATGACCGAGCAGCGAGATTCAGTTCTGTGTGTGTGTGTGTGTGTGTGTGTGT 379
QY 361 attgactctatgagcagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 420
DB 380 ATTGACTCTATGAGCAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 439
QY 421 gactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 480
DB 440 GAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 499
QY 481 tgaagatcttcatgtactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 540
DB 500 TGAAGATCTTCATGTACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 559
QY 541 gaagcagtagagggcccttgacactcaagttctctgtgtgtgtgtgtgtgtgtgtgtgt 600
DB 560 GAAAGCAGTAGAGGCCCTCGACACTCATGTTCTTCGCTTTCCTGTATGATGAGCTGT 619
QY 601 ccgtgcccaatgagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 660
DB 620 CCTGTCCCATGAGGTCTGTACTTAAAGGAGCTGAGCTGAGTGGCTTACATGAGGAGCT 679
QY 661 gctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 720
DB 680 GTCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 739
QY 721 gcccctcatgtagatctcttagatgacactcccaatccctcatcaccaccagagatgt 780
DB 740 GCCCCTCATGAGATCTTCTAGATGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 799
QY 781 gttgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 840
DB 800 GTTGCCAGCCAGGCTCCAGCAGCCAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 859
QY 841 aagcagtagttcagttttaaagatgacatlaagaggaaccagctcgtgtgtgtgtgtgt 900
DB 860 AGGAGAGGTGCTGGTTTAAAGATGAGCTTAAAGAGGAGGAGCCAGCTGAGTGTGAGCT 919
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DB 920 ATGTCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 979
QY 961 agcaatgtacacagcagcctcagtagcccatctcagcagtagtgagtagcagtagtagtg 1020
DB 980 AGCAATGTACACGAGCCTCAGTAGAGCCCATCTGACAGTGTGTGTGTGTGTGTGTGTGT 1039

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DB 1040 GTTGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1099
QY 1081 aagtgacctcagcagtagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1140
DB 1100 AAGTGACCTCAGCAGTACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1159
QY 1141 aaaaaaaaaa 1152
DB 1160 AAAAAAAAAA 1171

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RESULT 3
AB035343 3144 bp mRNA PRI 12-DEC-2000
LOCUS
DEFINITION
Homo sapiens TCl6f4 mRNA for T-cell leukemia/Lymphoma 6 ORF105,
T-cell leukemia/Lymphoma 6 ORF72, complete cds, clone:pdG4.
ACCESSION
AB035343
VERSION
AB035343.1 GI:8176590
KEYWORDS
T-cell leukemia/Lymphoma 6 ORF72; TCl6f4; T-cell leukemia/Lymphoma
6 ORF105.
SOURCE
Homo sapiens cell_line:Daudi cDNA to mRNA, clone:pdG4.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 3144)
Salton M., Sugimoto J., Hatakeyama T., Russo G. and Isobe M.
Identification of the TCl6 genes within the breakpoint cluster
region on chromosome 14q32 in T-cell leukemia
Oncogene 19 (23), 2796-2802 (2000)
20309940
JOURNAL
Oncogene 19 (23), 2796-2802 (2000)
MEDLINE
2 (bases 1 to 3144)
REFERENCE
Isobe M., Salton M. and Sugimoto J.
Direct Submission
Submitted (29-NOV-1999) to the DDBJ/EMBL/Genbank databases.
Masaharu Isobe, Toyama University, Materials and Biosystem
Engineering, Faculty of Engineering, 3190 Gofuku, Toyama 930-8555,
Japan (E-mail: isobe@eng.toyama-u.ac.jp., Tel: +81-76-445-6872,
Fax: +81-76-445-6874)
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 Query Match 83.6%; Score 963; DB 9; Length 3144;


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Oy 670 ctgagcagcttccctgctgctgagcctggtgtcttctctctgtgcccctcat 729
Db 3050 ctgagcagcttccctgctgctgagcctggtgtcttctctctgtgcccctcat 3109
Oy 730 gctgactctctagaatgcaactcccaatccctctcataccaacaggaatgtgtcccaag 789
Db 3110 gctgactctctagaatgcaactcccaatccctctcataccaacaggaatgtgtcccaag 3169
Oy 790 caagcctccagcaccacagctgagctgctgtaattggaactacatccatggaagcagatg 849
Db 3170 caagcctccagcaccacagctgagctgctgtaattggaactacatccatggaagcagatg 3229
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Db 3230 ttgcggttaagaagatgagcattagaagagcccaactctgagctgagcttgatgcccctgt 3289
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Oy 1090 tcaagctactggttaataaacttattgtctcactgtgtcaaaaaaataaaaaaataaaaaa 1149
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Oy 1150 aaa 1152
Db 3530 aaa 3532

RESULT 6
AB035341 3599 bp mRNA PRI 12-DEC-2000
LOCUS Homo sapiens TCl6f2 mRNA for T-cell leukemia/lymphoma 6 ORF141,
DEFINITION T-cell leukemia/lymphoma 6 ORF72, complete cds, clone:PDG2.
ACCESSION AB035341
VERSION AB035341.1 GI:8176584
KEYWORDS T-cell leukemia/lymphoma 6 ORF72; TCl6f2; T-cell leukemia/lymphoma
6 ORF141.
SOURCE Homo sapiens cell_line:Daudi CDNA to mRNA, clone:PDG2.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 3599)
AUTHORS Saitou,M., Sugimoto,J., Hatakeyama,T., Russo,G. and Isobe,M.
TITLE Identification of the TCl6 genes within the breakpoint cluster
region on chromosome 14q32 in T-cell leukemia
JOURNAL Oncogene 19 (23), 2796-2802 (2000)
MEDLINE 20309940
REFERENCE 2 (bases 1 to 3599)
AUTHORS Isobe,M., Saitou,M. and Sugimoto,J.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-1999) to the DDBJ/EMBL/GenBank databases.
Masaharu Isobe, Toyama University, Materials and Biosystem
Engineering, Faculty of Engineering, 3190 Gofuku, Toyama 930-8555,
Japan (E-mail:isobe@eng.toyama-u.ac.jp., Tel:+81-76-445-6872,
Fax:+81-76-445-6874)
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3310..3528
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AOKGAWRDFGLCFCLFSPSAGRDASP"
BASE COUNT 883 a 926 c 914 g 876 t
ORIGIN
Query Match 83.6%; Score 963; DB 9; Length 3599;
Best Local Similarity 100.0%; Pred. No. 3e-255;
Matches 963; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 190 tatgaaccacatcaccagctgactgtgagagatgagctgacatccaggagctactc 249
Db 2637 TATGACCACATCACAAGTGCATTGTGGCAGATGCGAGTGCATACCCGGAGCTACTC 2696
Oy 250 tctctcgagcagatgacctctcccaagctgcccgtgtgtgacacttaccacggagag 309
Db 2697 TCCTCCGGCAGATGCCCTTCTCCAGCTGCCCGCTGTGGACCTCTACCCGGGAGG 2756
Oy 310 aagtaacagagcagctgactcagcttctcgggaataagcagaccatgagcagatgactct 369
Db 2757 AAGTACGAGCAGCGGATTCAGATTCTGGGAATACAGACCATGCGCAGATTGACTCT 2816
Oy 370 atggagcagctggtctcaacataatagcagagagagaaagactgacactggagatgctg 429
Db 2817 ATGGAGCAGCTGGTCTTAACATATACGCCGAGAGAAAGACTGACATGSGAGTGGCTG 2876
Oy 430 gccctgctgagccctgacctctcttgagcctggtgtctcctcaatgccccctcagtgagatct 489
Db 2877 GCCCTGCTGAGCCCTGCTTCTTGAGCTGTGTCTCCTCATGCCCTCACTGAGATCT 2936
Oy 490 tcatgactgctcttctctctgttggacaccagagatagcctcttgcaagcagaagcagt 549
Db 2937 TCATGACTGCTCTCTCTGTGGTGGACACCCAGCATACCTCTTGACAGCAGAGCAGT 2996
Oy 550 agggccctgagacactcagttctctcgtttcctttagatcagatccctgctgtccca 609
Db 2997 AGGGCCCTGAGACCTAGATTCTCTGCTTCTCTTATACATCTCTGCTGCCCTGCCA 3056
Oy 610 ctgagctgacttgaagagagctgagctgagctgagctgagctgagctgagctgagctgag 669
Db 3057 CTGAGCTGCTGACTTGAAGAGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 3116
Oy 670 ctgagcagcttccctgctgctgagcctggtgtcttctctctgtgcccctcat 729
Db 3117 CTGAGCAGCTTCCCTGCTGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 3176
Oy 730 gctgactctctagaatgcaactcccaatccctctcataccaacaggaatgtgtcccaag 789
Db 3177 GCTGACTCTTGAATGCACTCCCAATCCCTTCAACCCACAGAGATGTGTCCCAAG 3236
Oy 790 caagcctccagcaccacagctgagctgctgtaattggaactacatccatggaagcagatg 849

```


RESULT 11
AF110467 1248 bp DNA PRI 18-MAR-1999
LOCUS Homo sapiens T-cell leukemia/Lymphoma 1B (TCL1B) pseudogene,
DEFINITION complete sequence.
ACCESSION AF110467
VERSION AF110467.1 GI:4324706
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 1248)
AUTHORS Pekarsky Y., Hallas C., Isobe M., Russo G. and Croce C.M.
TITLE Abnormalities at 14q32.1 in T cell malignancies involve two
oncogenes
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (6), 2949-2951 (1999)
MEDLINE 99178995
REFERENCE 2 (bases 1 to 1248)
AUTHORS Pekarsky Y., Hallas C. and Croce C.M.
TITLE Direct Submission
JOURNAL Submitted (02-DEC-1998) KCL, Thomas Jefferson University, 233 South
10th Str. BLSR 1032, Philadelphia, PA 19107, USA
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/db_xref="taxon:9606"
/chromosome="5"
/map="5q12-q13"
163..1248
/gene="TCL1B"
/note="T-cell leukemia/Lymphoma 1B"
BASE COUNT 263 a 361 c 312 g 312 t
ORIGIN
Query Match 60.8%; Score 700.4; DB 9; Length 1248;
Best Local Similarity 81.5%; Pred. No. 1.2e-182;
Matches 928; Conservative 0; Mismatches 156; Indels 54; Gaps 8;
QY 2 aggcgggtcccggtgacgaacttcgaactgctcgaagcttcgtgctcgaagtgc 61
DB 149 AGGGGACCCAGAGTCACACCTTGCATGCGCTCCCAAGCTTCCGCACTCCAGGAC 208
QY 62 cccctggg--cgctcgtgacccagagcctgagccttcaagaatgaagagagagac 119
DB 209 CCCCCCAACTGTCGTGTGATCTGAGACCTGSCATCTATGAGGATGACAAAGGAGGAC 268
QY 120 ctgggtgactcgtgctggtggttcaatccctcgtgtaggaatggcagag-----gc 173
DB 269 CTGGGTACTCTGTGTGTCGCTCACTCCCTGCAACAGAGAGAGGCGCGCTCAAG 328
QY 174 ctccagagcagacatgaaccacacacagctgacactgtgacagatgacagtgca 233
DB 329 CTCCAGGCGACATATGAACTACACATGACAGTGCACATGATGAGATGCCAGTGC 388
QY 234 taccggagacactctctcctcggcagagatcccttcccaagctgcgcggtgtgca 293
DB 389 CACCGGGAACACCTCTCCACGACGCTGCCCTTCTCCCACTCTCCGCTGGCA 448
QY 294 gctctacccggaggaagtaacagacagcagtgatccagttctctggaataagcagaca 353
DB 449 GCTTACCCCAAGAGAGGATCAACAGCAATTCAGTTTCTGGAAATAGTGGA--- 505
QY 354 tggcgaattgactcattgagcagcgtgctcctaataatataccggaaggaagagatg 413
DB 506 ---CGAATGCTCTCATGAGACAGCTGCTCTTACATATTGGCCGCAAGGAATACG 562
QY 414 acaactggagatgctggtccctcgtgctcctctcctcgtggtgtcctcctatgccc 473
DB 563 A-----CTCCTCTGGGCTCATGCTCTCTTCTGGGCGC 591

QY 474 cctcagtgagatctcattgacacgtctctctgtgttgacacccagatagctcctt 533
DB 592 CCTCATGTAGGATCTTGTGTACTGATTCCTGTTGCACACCCAGCGTGCCTCTT 651
QY 534 gcaagagagagcagtagggccctcagacacagttctctctgtttcttagtttca 593
DB 652 GCAAGCAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 711
QY 594 gtccctgtcctccactcaggtctgacttaggagcagctgagcctgagtggtcact- 652
DB 712 GTCTGTGCTGCTTCCATCATGATCTACACTGAGGAGGAGGAGGAGGAGGAGGAG 771
QY 653 ggggcccctctgt- 710
DB 772 GGGGCCCCGTCTGTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 831
QY 711 tctctctgtccctcactgtgacttctctagatgacactcccaateccctt-----ca 765
DB 832 TCTCTCTGTGCTTCCATCATGATCTACACTGAGGAGGAGGAGGAGGAGGAGGAG 891
QY 766 taccacacagatgt 825
DB 892 TACCCACAGGCTTCTCATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 951
QY 826 aaactcaacacagcagcagtggttgcgttgaagatgacatagagagagagagc 885
DB 952 GAACTCAGCATGAGCAGTCACTGCTGCTTTAGAGAGGAGGAGGAGGAGGAGGAG 1011
QY 886 tggatgtgagatgagcctcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 945
DB 1012 CGATGTGCTGCTTGTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1071
QY 946 atccagtgctgagcagcagatgtacacagcagcagcagcagcagcagcagcagc 1005
DB 1072 ATTAAGTCTGAGCAGCAGTCACTGCTGCTTTAGAGAGGAGGAGGAGGAGGAG 1131
QY 1006 agcatgagagatgagtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1065
DB 1132 AGCGTGAAGGATGAGGTTGGCTTATGCTTGTGCTTGTGCTTGTGCTTGTGCT 1190
QY 1066 ggtatgctagtcgtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 1123
DB 1191 GGATGTAATTCATGAAAGTCACTGCTGCTTGTGCTTGTGCTTGTGCTTGTGCT 1248

RESULT 12
CNS01DX2 166308 bp DNA PRI 26-APR-2001
LOCUS Human chromosome 14 DNA sequence BAC R-164H13 of library RPCT-11
DEFINITION from chromosome 14 of Homo sapiens (Human), complete sequence.
ACCESSION AL139020
VERSION AL139020.5 GI:13539193
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 166308)
AUTHORS Belling R., Petit J.L., Vico V., Dasilva C., Robert C., Wincker P.,
Brotlier P., Cactolico L., Barbe V., Pelletier E., Artiguenave F.,
Levy M., Beckenbergh R., Bruns T., deBerardinis V., Cruaud C.,
Gyapay G., Saurin W. and Weissenbach J.
TITLE Sequencing of the human chromosome 14
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 166308)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (26-APR-2001) Genoscope - Centre National de Sequencage :
BP 191 91006 Evry Cedex - FRANCE (E-mail : seque@genoscope.cns.fr
on Web : www.genoscope.cns.fr)
COMMENT On Apr 3, 2001 this sequence version replaced g1:12274871.
----- Genome Center
Center: Genoscope / Centre National de Sequencage

[illegible]

REFERENCE

1 (sites)

Fri Nov 30 11:03:03 2001

us-09-526-329-38.rge

Page 16

QY 675 ccagttccctctgctgagctgcaagctgtgggttc--ttctctctctgtgccctcatgct 732
 CC |||||||
 CC 324 ccggttccctctgctgctgcaagctgtgttcttctctctctctgccccctcatgct 383
 CC |||||||
 QY 733 gactctctagatgctccatcccaatccctt-----cataccacagagatgtgtgccca 787
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 CC 384 gactctctagatgctccatcccaatcccttctctctctctctcatccacccagctcatgccca 443
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 QY 788 gccagctctcagcagcccccagctgagctgtgattggaatactccatctgagcagcact 847
 CC |||||||
 CC 444 ccagagctctcagcagcccccagctgagcagctgtggaatactccatccacagcagcact 503
 CC |||||||
 QY 848 ggttcgtttaaagatgagcaltagaagagccagctctggaatgtgagcttgatgccct 907
 CC |||||||
 CC 504 ggttcgtttaaagatgagcagcagaggaactgtgtccctgtatgtgagcttgatgccct 563
 CC |||||||
 QY 908 ggttcgtttaaagatgagcagcagaggaactgtgtccctgtatgtgagcttgatgccct 967
 CC |||||||
 CC 564 ggttcgtttaaagatgagcagcagaggaactgtgtccctgtatgtgagcttgatgccct 622
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 QY 968 tacacgcagagctcagctgagcagcagctgacagctgagagagcagctgagagatgagct 1022
 CC |||||||
 CC 623 tatgctgagagctcagctgagcagcagctgacagctgagagagcagctgagagatgagct 676
 CC |||||||

RESULT 4

AAA89670 standard; cDNA; 561 BP.

AAA89670;

08-JAN-2001 (first entry)

Human T cell leukemia/Lymphoma 1 nucleotide sequence.

XX Exocytosis pathway protein; Exo protein; antiparkinsonian; antidiabetic;
 KW antiallergic; antidiabetic; noctropic; neuroprotective; anticonvulsant;
 KW vulnery; asthma; inflammation; allergy; Chediak-Higashi syndrome; CNS;
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease; diabetes;
 KW digestion disorder; wound healing disorder; gene therapy; ss.

OS Homo sapiens.

PN W0200043419-A2.

PD 27-JUL-2000.

PF 20-JAN-2000; 2000WO-US01431.

PR 20-JAN-1999; 99US-0116534.

PR 26-JAN-1999; 99US-0117274.

PR 26-JAN-1999; 99US-0117308.

PR 26-JAN-1999; 99US-0117309.

PR 26-JAN-1999; 99US-0117312.

PR 01-FEB-1999; 99US-0118177.

PR 01-FEB-1999; 99US-0118178.

PR 01-FEB-1999; 99US-0118179.

PR 09-FEB-1999; 99US-0119286.

PR 11-FEB-1999; 99US-0119998.

PR 11-FEB-1999; 99US-0119759.

XX (RIGF-) RIGEL PHARM INC.

XX LNO Y;

XX WPI; 2000-482908/42.

XX New nucleic acids encoding Exo proteins which are useful in the

PT diagnosis, treatment or prevention of exocytosis-mediated disorders

PT such as asthma, inflammation and allergies -

XX 14-SEP-2000; 2000US-0662191.

XX 19-OCT-2000; 2000US-0693036.

PS Disclosure; Page 251; 305pp; English.

XX The present sequence encodes a polypeptide which is associated with
 CC the exocytosis pathway. cDNA molecules encoding proteins involved in
 CC exocytosis have been isolated by yeast one-hybrid and two-hybrid
 CC screening. Novel proteins, termed Exo proteins, have been identified that
 CC interact with known exocytosis-associated proteins such as GS27, alpha
 CC snap, unc18-1, vamps, snap-23, and the rab family of proteins.
 CC Exo proteins and their agonists and antagonists are useful in the
 CC diagnosis, treatment or prevention of exocytosis-mediated disorders
 CC such as asthma, inflammation, allergies, Chediak-Higashi Syndrome
 CC (CHS), Alzheimer's disease, Parkinson's disease, Huntington's disease,
 CC diabetes, digestion disorders and wound healing disorders.
 CC The nucleic acids, antagonists or agonists of Exo proteins are useful
 CC in gene therapy. The nucleic acids are also useful for generating
 CC transgenic or knock-out animals which can be used in the
 CC development and screening of therapeutically useful reagents.

XX Sequence 561 BP; 110 A; 160 C; 151 G; 135 T; 5 other;

Query Match 5.5%; Score 62.8; DB 21; Length 561;

Best Local Similarity 57.7%; Pred. No. 3.4e-07;

Matches 112; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

QY 208 gtccactgttgagagatgagcagctgacatccggagagctactctctccggcagatgcc 267

DB 87 ggtccttgctgagagagagcgtgctcctgagagagcctatgagccaccacagatagac 146

QY 268 ttctccagagctgagcagcgtgtgagcagcttaccgccggagagctacagcagcagat 327

DB 147 ccaagcctgctgctatcatgtgagcagcttaccctgagagcagcagcagcagcagc 206

QY 328 tccagcttctggaataagcagacatgagcagatgagctctatgagcagcgtgtgctca 387

DB 207 tccagcttctgagcagctgagcagcagcagcagcagcagcagcagcagcagcagc 266

QY 388 acatacagcagcag 401

DB 267 gagctgctgagcagcag 280

RESULT 5

AA160765 standard; cDNA; 1235 BP.

AA160765;

22-OCT-2001 (first entry)

Human polynucleotide SEQ ID NO 4754.

XX Human; noctropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokine; thymolytic; drug screening; arthritis; inflammation;
 KW leukemia; ss.

OS Homo sapiens.

PN W0200153312-A1.

PD 26-JUL-2001.

PF 26-DEC-2000; 2000WO-US34263.

PR 21-JAN-2000; 2000US-0488725.

PR 25-APR-2000; 2000US-0552317.

PR 09-JUL-2000; 2000US-0598042.

PR 19-JUL-2000; 2000US-0620312.

PR 03-AUG-2000; 2000US-0653450.

PR 14-SEP-2000; 2000US-0662191.

PR 19-OCT-2000; 2000US-0693036.

CC increased expression of TcL-1 proteins and/or with chromosome 14
CC abnormalities, esp. T-cell Leukemia and Lymphoma.

XX
SQ Sequence 4922 BP; 1091 A; 1278 C; 1168 G; 1202 T; 183 other;

Query Match 4.3%; Score 50; DB 17; Length 4922;
Best Local Similarity 57.4%; Pred. No. 0.0023;
Matches 89; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

OY 208 gtgcactgtgagatgagatgacatgacacgagagactctctccgagcagatgccc 267
DB 2228 gtgctctgtcgaggaagacgctgcgggagacatagacccacacagatagc 2287
OY 268 ttctccacatgcccgcgtgtgacgactacacccggaggaagacagcagcagc 327
DB 2288 ccaagcctgtgcctatcatatggtgacgactacacctgagacgataccgactcagc 2347
OY 328 tccagttctgggaatagacagacatgagcagat 362
DB 2348 tccagttctggcgttagtgtacacatcaagat 2382

RESULT 9
AA10594/c
ID AA10594 standard; DNA: 10732 BP.

XX AA10594;

DT 29-JUN-2000 (first entry)

XX Gene encoding a subunit of cellulose synthase.

XX Cellulose synthase; cellulose production; increase yield; ds.

XX Vigna angularis.

XX JP2000060568-A.

XX 29-FEB-2000.

XX 26-AUG-1998; 98JP-0239998.

XX 26-AUG-1998; 98JP-0239998.

XX (MIZU) MIZUNO K.

XX (OJIP) OJI PAPER CO.

XX WPI, 2000-342371/30.

XX P-PDB: AAV85179.

XX A gene encoding a cellulose synthetic equipment - for the improvement

XX in the amount of cellulose synthesised in a plant body

XX Claim 2; Page 14-21; 32pp; Japanese.

XX This sequence represents a gene encoding a subunit of the cellulose

XX synthase complex of Vigna angularis. The invention relates to subunits of

XX cellulose synthetic equipment, that can be used to increase the amount of

XX cellulose synthesised by a plant. The proteins and genes encoding them

XX can also be used to improve the properties of the cellulose being

XX produced by a plant.

XX Sequence 10732 BP; 3149 A; 1212 C; 2074 G; 2046 T; 2251 other;

Query Match 4.0%; Score 45.6; DB 21; Length 10732;
Best Local Similarity 13.2%; Pred. No. 0.047;
Matches 68; Conservative 21; Mismatches 238; Indels 0; Gaps 0;

OY 419 gggagtgctgagcgcctgctgctctctgagcgtggtctctatgcccccc 478
DB 10134 SRSRTSTCTAKYSTYSTSTNCSDSGDNSTAKYSTTTTAYDAKCTTNTSTCTR 10075

OY 479 agtggagatctcatgactgctctctctgtttgacacccagacatagcctcttgagg 538
DB 10074 ASTYDASRRCISSTYKASRGBSDDCTBSRSCSYDASRYANCTBCYTTBAKYRARC 10015
OY 539 cagaagcagtagtaggcccctgacacactcagttctctctgtttcttactatagtcct 598
DB 10014 YDAVARCNSSTRYAAVSDSTCYTRCSCRNCYSTYSSSTYASTTBTTCYTCRCS 9955
OY 599 gtctgtccactcagtgctgacttaggagcagctgagcgtgagtggtcttccagggcc 658
DB 9954 RCYSRSTCMNCISYCCYTSRYSSTTTSTCTCTTSTBTBTBTBTBTBTBTBTBTBT 9895
OY 659 ctgtctgtgtgtagccagcttccctgctgctgagcagcagtgtagtcttctctct 718
DB 9894 RGSDSKGNCTYNTNCYDASTSDTBYSRCYVSYSTSDSTSTSTSTSTSTSTSTST 9835
OY 719 gtgcccctcatgctatctctagatgacactcccaatccctctacacacagagat 778
DB 9834 BSRSTSDSTSTYRCSDSDYDATABSDNSTMCCYDASRTBTBTBTBTBTBTBTBTBT 9775
OY 779 gtgtgcccagcagagcctccagacacccagctgagctgtagtggaactcaacatg 838
DB 9774 TTSRGTDMNSTSRYSSTYSSTYSSTYSSTYSSTYSSTYSSTYSSTYSSTYSST 9715
OY 839 gcagcagtggtgtcgttttagagatgacatagagagagcagctgtagtggact 898
DB 9714 SSSHTYBVCNRCCCYDAYSCTSRDARCYDACSNSCTYDNTBTSTSTSTSTST 9655
OY 899 ggtgcccctgtggtatcagttctgtgacacttgg 935
DB 9654 NCYDATTSTCTBT 9618

RESULT 10
AAV84490
ID AAV84490 standard; DNA: 1533 BP.

XX AAV84490;

DT 01-MAR-1999 (first entry)

XX Human secreted protein gene 80 clone HNF4E54.

XX Human; secreted protein; fusion protein; gene therapy; protein therapy;
XX diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukemia;
XX developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
XX immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
XX inflammation; ischaemic shock; Alzheimer's disease; osteoarthritis; AIDS;
XX cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
XX osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
XX endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.

XX Homo sapiens.

XX WO9854963-A2.

XX 10-DEC-1998.

XX 04-JUN-1998; 98MO-US11422.

XX 18-DEC-1997; 97US-0070923.
XX 06-JUN-1997; 97US-0048877.
XX 06-JUN-1997; 97US-0048881.
XX 06-JUN-1997; 97US-0048884.
XX 06-JUN-1997; 97US-0048893.
XX 06-JUN-1997; 97US-0048896.
XX 06-JUN-1997; 97US-0048899.
XX 06-JUN-1997; 97US-0048915.
XX 06-JUN-1997; 97US-0048949.
XX 06-JUN-1997; 97US-0048964.
XX 06-JUN-1997; 97US-0048972.
XX 06-JUN-1997; 97US-0049020.

PT	New isolated human genes and the secreted polypeptides they encode -
PT	useful for diagnosis and treatment of e.g. cancers, neurological
PT	disorders, immune diseases, inflammation or blood disorders
XX	
PS	Claim 4: Page 343; 772pp; English.
XX	
CC	The invention relates to nucleic acid sequences (AAV84411 to AAV84633)
CC	encoding human secreted proteins (AAW8534 to AAW8756). The secreted
CC	protein gene sequences are deposited with the ATCC under deposit numbers
CC	ATCC 97974, 97974, 97975, 97976, 97977, 209007, 209008, 209009, 209010,
CC	209011, 209080, 209081, 209082, 209083, 209084, 209085, 209511. Host
CC	cells comprising recombinant vectors containing the nucleic acid
CC	sequences are used for the recombinant production of the secreted
CC	proteins. The polynucleotide and amino acid sequences are useful for are
CC	useful for preventing, treating or ameliorating medical conditions e.g.
CC	by protein or gene therapy. Pathological conditions can be also
CC	diagnosed by determining the amount of the new polypeptides in a sample
CC	or by determining the presence of mutations in the new polynucleotides.
CC	Specific uses are described for each of the polynucleotides, based on
CC	which tissues they are most highly expressed in, and include developing
CC	products for the diagnosis or treatment of cancer, neurodegenerative
CC	disorders, developmental abnormalities and foetal deficiencies, blood
CC	disorders, tumours, leukemias, diseases of the immune system, autoimmune
CC	diseases, hepatic and renal disease, lymphomas, inflammation, allergies,
CC	ischemic shock, Alzheimer's and cognitive disorders, schizophrenia,
CC	restenosis, prostate diseases, obesity, disorders involving osteoclasts
CC	such as osteoporosis, arthritis or malignancies, diseases of testes,
CC	lung or thymus, digestive/endocrine disorders, infections and AIDS. The
CC	polypeptides are also useful for identifying their binding partners.
CC	The present sequence represents a gene encoding a human secreted protein
CC	(see descriptor line for gene number and clone identification).
XX	
SQ	Sequence 1533 BP; 272 A; 454 C; 495 G; 302 T; 10 other:
XX	
Query Match	3.6%; Score 41.6; DB 20; Length 1533;
Best Local Similarity	53.0%; Pred. No. 0.25;
Matches	89; Conservative 0; Mismatches 79; Indels 0; Gaps
Oy	985 gagccatctgcacagctggggagcctgaggagtggttgcctcgtcgtctctatt 1044
Db	1354 gagcatagcttggggggagcagccacgaatgaagcctcgttgtaagaccagctgct 1413
Oy	1045 cagtcctcagctacaggaagagatgcagtcgcgtaagagtgacctcaagtaactggtta 1104
Db	1414 gggccacagctcctatgtaagcctctcattggttctctagaaccaccacccagcaaca 1473
Oy	1105 attaaacttatctgcactgcacaaataaaaaaaataaaaaaa 1152
Db	1474 aatccaataagagacatcccaaaaaataaaaaaaataaaaaa 1521
RESULT	11
AAAD04477	
ID	AAAD04477 standard; cDNA: 1719 BP.
XX	
XX	AAAD04477;
AC	
XX	
DT	04-JUL-2001 (first entry)
XX	
DE	Human sphingosine kinase type 1 (hsk1) cDNA.
XX	
XX	Human; sphingosine kinase type 1; SK1; chromosome 17q25.2;
KM	sphingosine-1-phosphate; SIP; drug screening; therapy; hamostasis;
KM	thrombosis; allergic reaction; proliferative disease; cancer; stroke;
KM	haemolytic disorder; leukemia; cardiovascular disease; diabetes;
KM	atherosclerosis; coronary artery disease; dyslipidaemia; diabetes;
KM	autoimmune disease; inflammatory disease; multiple sclerosis;
KM	T helper-1 related disease; chronic obstructive pulmonary disease;
KM	asthma; myocardial infarction; neurodegenerative disorder;
KM	wound healing; embryogenesis; anticoagulant; cerebroprotective;
KM	neuroprotective; antipsoriatic; antiarthritic; cyostatic; cardiac;
KM	vulneraty; ss.

	RESULT	13
	AACT77441	
ID	AACT77441	standard; cDNA; 2440 BP.
XX		
AC	AACT77441;	
XX		
DT	08-FEB-2001	(first entry)
XX		
DE	Human OREF2996	polynucleotide sequence SEQ ID NO:5991.

CC	pathological conditions associated with an ORFX-associated disorder. The
CC	the presence of or predisposition to, or preventing or treating
CC	antihyproid; and antianemic. The sequences can be used for determining
CC	antiinflammatory; antibacterial; antiviral; antifungal; antipneumatic;
CC	antidiabetic; hypotensive; dermatologic; immunosuppressive;
CC	immunostimulant; cardiant; thrombotytic; coagulant; vasotropic;
CC	osteoplastic; antiparkinsonian; neurotropic; neuroprotective;
CC	antisporadic; antiparkinsonian; neotrophic; hepatrotropic;
CC	sequences have activities such as: cytostatic; hepatrotropic; vulnary;
CC	which represent the human ORFX open reading frames 1 to 3161. The ORFX
XX	AAC74446 to AAC77606 encode the proteins given in AAB43397,
PS	Claim 5; Page 5164-5166; 5507pp; English.
XX	
XX	
PT	Novel nucleic acids and peptides derived from open reading frame X,
PT	useful for treating e.g. cancers, proliferative disorders -
PT	neurodegenerative disorders and cardiovascular disease -
XX	P-PSDB; AAB43232.
DR	WPI: 2000-602362/57.
DR	
XX	
PA	(CURA-) CURAGEN CORP.
PR	
PR	30-MAR-2000: 2000US-0540763.
PR	05-APR-1999: 99US-0127728.
PR	02-APR-1999: 99US-0127636.
XX	31-MAR-1999: 99US-0127607.
PF	31-MAR-2000: 2000WO-US08621.
PD	
XX	
XX	
PN	WO200058473-A2.
XX	
OS	Homo sapiens.
KM	thrombosis; contraceptive; ss.
KM	bone damage; cartilage damage; antiinflammatory disease; coagulation;
KM	allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
KM	severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
KM	cholesterol ester storage; systemic lupus erythematosus; infection;
KM	cardiovascular disease; diabetes mellitus; hypothyroidism; scid; AIDS;
KM	neurodegenerative disorder; osteoarthritis; graft vs host disease;
KM	antianemic; gene therapy; cancer; proliferative disorder; hypertension;
KM	antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
KM	hypotensive; dermatologic; immunosuppressive; antiinflammatory;
KM	immunostimulant; thrombotytic; coagulant; vasotropic; antidiabetic;
KM	anticonvulsant; osteopathic; antarthritic; immunosuppressant; cardiant;
KM	vulnary; antiparitic; antiparkinsonian; neotrophic; neuroprotective;
KM	Human; open reading frame; ORFX; detection; cytosolic; hepatrotropic;
KM	
XX	

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Query Match      3.5%; Score 40.4; DB 21; Length 2440;
Best Local Similarity 80.0%; Pctd. No. 0.63;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1103 taattaaactttatgtcgcacgtcaaaaaaaaaaaaaaaaaaaaaa 1152
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2370 taataaatctttatgtgcacgtcaaaaaaaaaaaaaaaaaaaaaa 2427

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RESULT	14
AAH34812	
ID	AAH34812 standard; cDNA: 2617 bp.
AC	AAH34812;
DT	03-SEP-2001 (first entry)
DE	Human colon cancer antigen encoding cDNA SEQ ID NO:1894.
XX	
XX	Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW	colorectal carcinoma; chromosome 7; ss.
XX	
XX	Homo sapiens.
OS	
PN	WO200122920-A2.
PD	
PD	05-APR-2001.
XX	
XX	28-SEP-2000; 2000WO-US26524.
XX	
PR	29-SEP-1999; 99US-0157137.
PR	03-NOV-1999; 99US-0163280.
XX	
XX	(HUMA-) HUMAN GENOME SCI INC.
PA	
PI	
PI	Ruben SM, Barash SC, Blirise CE, Rosen CA;
XX	
DR	WPI; 2001-235357/24.
DR	P-PSDB; AAG75407.
XX	
XX	Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
PT	useful for preventing, diagnosing and/or treating colorectal cancers -
XX	
PS	Claim 1; Page 3407-3408; 9803pp; English.
XX	
XX	AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
CC	cancer-associated nucleic acid molecules (N) and proteins (P), where
CC	the proteins are collectively known as colon cancer antigens. The colon
CC	cancer antigens have cytoskeletal activity and can be used in gene
CC	therapy and vaccine production. N and P may be used in the prevention,
CC	diagnosis and treatment of diseases associated with inappropriate P
CC	expression. For example, N and P may be used to treat disorders
CC	associated with decreased expression by rectifying mutations or deletions
CC	in a patient's genome that affect the activity of P by expressing
CC	inactive proteins or to supplement the patients own production of P.
CC	Additionally, N may be used to produce the colon cancer-associated Ps,
CC	by inserting the nucleic acids into a host cell and culturing the cell
CC	to express the proteins. N and P can be used in the prevention, diagnosis
CC	and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204

Fri Nov 30 11:03:05 2001

us-09-526-329-38.rng

Page 12

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: November 29, 2001, 04:06:24 ; Search time 194.7 Seconds

(Without alignments)
1340.024 Million cell updates/sec

Title: US-09-526-329-38

Perfect score: 1152

Sequence: 1 gagcgcgccgcgttgag.....aaaaaaaaaaaaaaaa 1152

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 351203 seqs, 113238999 residues

Total number of hits satisfying chosen parameters: 702406

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/prodata/2/ina/5A.COMB.seq:*
2: /cgn2_6/prodata/2/ina/5B.COMB.seq:*
3: /cgn2_6/prodata/2/ina/6A.COMB.seq:*
4: /cgn2_6/prodata/2/ina/6B.COMB.seq:*
5: /cgn2_6/prodata/2/ina/PCUS.COMB.seq:*
6: /cgn2_6/prodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	64.4	5.6	7218	1 US-08-232-463-14	Sequence 14, Appl
2	62.8	5.5	1324	2 US-08-330-272-1	Sequence 1, Appl
3	62.8	5.5	1324	5 PCT-US95-13663-1	Sequence 1, Appl
4	50	4.3	4922	2 US-08-330-272-5	Sequence 5, Appl
5	50	4.3	4922	5 PCT-US95-13663-5	Sequence 5, Appl
6	38.8	3.4	1817	1 US-08-473-981A-5	Sequence 5, Appl
7	38.6	3.4	1817	2 US-08-474-087-5	Sequence 5, Appl
8	38.6	3.4	284	4 US-09-040-984-80	Sequence 80, Appl
9	37.6	3.3	2017	4 US-09-436-983-1	Sequence 80, Appl
10	37.2	3.2	1781	1 US-08-314-615-2	Sequence 2, Appl
11	37.2	3.2	1781	1 US-08-314-362-2	Sequence 2, Appl
12	37.2	3.2	1781	1 US-08-433-010-2	Sequence 2, Appl
13	37.2	3.2	1781	1 US-08-245-295-4	Sequence 2, Appl
14	37.2	3.2	1781	1 US-08-481-130-4	Sequence 4, Appl
15	37.2	3.2	1781	1 US-08-656-984A-4	Sequence 4, Appl
16	37.2	3.2	1781	1 US-08-482-882-2	Sequence 2, Appl
17	37.2	3.2	1781	1 US-08-485-604-4	Sequence 2, Appl
18	37.2	3.2	1781	1 US-08-483-89-2	Sequence 2, Appl
19	37.2	3.2	1781	2 US-08-487-1130-2	Sequence 2, Appl
20	37.2	3.2	1781	2 US-08-487-595-4	Sequence 2, Appl
21	37.2	3.2	1781	2 US-08-473-503-2	Sequence 2, Appl
22	37.2	3.2	1781	2 US-08-483-932-2	Sequence 2, Appl
23	37.2	3.2	1781	3 US-08-720-420A-2	Sequence 2, Appl
24	37.2	3.2	1781	3 US-08-714-017-2	Sequence 2, Appl
25	37.2	3.2	1781	3 US-08-863-790-2	Sequence 2, Appl
26	37.2	3.2	1781	3 US-08-475-680-2	Sequence 2, Appl
27	37.2	3.2	1781	3 US-08-296-749-2	Sequence 2, Appl

c 28	37	3.2	289	4 US-09-007-005-17	Sequence 17, Appl
c 29	37	3.2	289	4 US-09-244-796-17	Sequence 17, Appl
c 30	37	3.2	322	4 US-09-385-982-216	Sequence 216, App
c 31	37	3.2	322	4 US-09-385-982-362	Sequence 362, App
32	36.6	3.2	4843	3 US-08-986-485-1	Sequence 1, Appl
33	36.4	3.2	570	1 US-08-469-667-13	Sequence 13, Appl
34	36.4	3.2	570	5 PCT-US95-07289-13	Sequence 13, Appl
35	36.4	3.2	1357	6 5340934-7	Patent No. 5340934
36	36.2	3.1	1394	1 US-07-730-953-1	Sequence 1, Appl
37	36	3.1	1147	1 US-08-665-716-1	Sequence 1, Appl
38	36	3.1	1385	1 US-08-405-392-1	Sequence 1, Appl
39	36	3.1	3385	3 US-08-487-681-1	Sequence 1, Appl
40	36	3.1	3385	3 US-08-666-221B-3	Sequence 1, Appl
41	36	3.1	3385	3 US-08-666-221B-9	Sequence 1, Appl
42	35.6	3.1	902	2 US-08-378-939-11	Sequence 9, Appl
43	35.4	3.1	703	4 US-09-313-300-6	Sequence 11, Appl
44	35.4	3.1	989	2 US-08-874-460-1	Sequence 6, Appl
45	35.4	3.1	2684	2 US-08-984-171-2	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHERFLINGER, F.
; APPLICANT: PARKER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESS: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZ9pt-F15
US-08-232-463-14

RESULT 8
US-09-040-984-80
Sequence 80, Application US/09040984
Patent No. 6210883
GENERAL INFORMATION:
APPLICANT: Need, Steven G.
APPLICANT: Wang, Tongtong
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS
TITLE OF INVENTION: OF LUNG CANCER
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: SPED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/040.984
FILING DATE: 18-MAR-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.456

TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
TELEFAX: 206-282-6031
TELEX:
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 284 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-040-984-80

Query Match 3.4%; Score 38.6; DB 4; Length 284;
Best Local Similarity 81.5%; Pred. No. 0.058;
Matches 44; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
Qy 1099 tggtaataacttattgtctcactgcataaaaaaaaaaaaaaaaaa 1152
Db 231 TTGGGAAATTAATGTTATTCTTCTGTGAAAAAATAAAAAAAAAA 284

RESULT 9
US-09-436-983-1
Sequence 1, Application US/09436983
Patent No. 6294343
GENERAL INFORMATION:
APPLICANT: MACK, David
APPLICANT: GISH, Kurt C
APPLICANT: WILSON, Keith E
TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSING COLORECTAL CANCER,
TITLE OF INVENTION: COMPOSITIONS, AND METHODS OF SCREENING FOR COLORECTAL
TITLE OF INVENTION: CANCER MODULATORS
FILE REFERENCE: A-68431/RMS/DAY
CURRENT APPLICATION NUMBER: US/09/436,983
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 2017
TYPE: DNA
ORGANISM: Homo sapiens
US-09-436-983-1

Query Match 3.3%; Score 37.6; DB 4; Length 2017;
Best Local Similarity 54.3%; Pred. No. 0.33;
Matches 76; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

Qy 1013 aggaatggtttggcgtctcttcttctcagctcctcagctcagaaggatgct 1072
Db 1872 atggaagaagactaggtcttcttcttctcagctcagctcagctcagct 1931
Qy 1073 agtccgtgaagtgacctcagctcagctcagctcagctcagctcagct 1132
Db 1932 tctgaagtttactgctcagctcagctcagctcagctcagctcagct 1991
Qy 1133 aaaaaaaaaaaaaaaaaa 1152
Db 1992 aaaaaaaaaaaaaaaaaa 2011

RESULT 10
US-08-314-615-2
Sequence 2, Application US/08314615
Patent No. 5525487
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Vazeux, Rosemay
TITLE OF INVENTION: I-CAM Related Protein
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

ADDRESSEE: Bicknell
STREET: Two First National Plaza, 20 South Clark
STREET: Street
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/314,615
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/827,689
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 27866/30704
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)946-5750
TELEFAX: (312)984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1781 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-314-615-2

Query Match 3.2%; Score 37.2; DB 1; Length 1781;
Best Local Similarity 63.3%; Pred. No. 0.4;
Matches 57; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

Qy 1063 aaggatgctagtcgtgaagtgacctcagctcagctcagctcagctcagct 1122
Db 1677 AAGTGGCGGCGGCTTGGCTCGCCCTCAGATTCGCAACATTAACCTCAACTCC 1736
Qy 1123 ctgtcaaaaaaaaaaaaaaaaaa 1152
Db 1737 CAAAAAATAAAAAAAAAA 1766

RESULT 11
US-08-314-362-2
Sequence 2, Application US/08314362
Patent No. 5532127
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Vazeux, Rosemay
TITLE OF INVENTION: I-CAM Related Protein
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: Two First National Plaza, 20 South Clark
STREET: Street
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/314,362
FILING DATE: 27-JAN-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/894,061
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 26-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 553212and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30918
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)346-5750
TELEFAX: (312)984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1781 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-314-362-2

Query Match 3.2%; Score 37.2; DB 1; Length 1781;
Best Local Similarity 63.3%; Pred. No. 0.4;
Matches 57; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

OY 1063 aaggagtgtagtcgcggaagtgacccacagctcgttaatttaattatgtctca 1122
DB 1677 AAGGTTGGGGGGGCTTGCTGCTCAAGATTCGCCACCAATTAAGCCTTCAACTCC 1736

OY 1123 ctgtcaaaaaaaaaaaaaaaaaaaaaa 1152
DB 1737 CAAAAAAMAAAAAAAAAAAAAAAAAAAAA 1766

RESULT 12
US-08-433-010-2
Sequence 2, Application US/08433010
Patent No. 5663293
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Vazeux, Rosemary
TITLE OF INVENTION: ICAM-Related Protein
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSER: Bicknell
STREET: Two First National Plaza, 20 South Clark
STREET: Street
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/433,010
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/009,266

FILING DATE:
APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5663293and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31218
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)346-5750
TELEFAX: (312)984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1781 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-433-010-2

Query Match 3.2%; Score 37.2; DB 1; Length 1781;
Best Local Similarity 63.3%; Pred. No. 0.4;
Matches 57; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

OY 1063 aaggagtgtagtcgcggaagtgacccacagctcgttaatttaattatgtctca 1122
DB 1677 AAGGTTGGGGGGGCTTGCTGCTCAAGATTCGCCACCAATTAAGCCTTCAACTCC 1736

OY 1123 ctgtcaaaaaaaaaaaaaaaaaaaaaa 1152
DB 1737 CAAAAAAMAAAAAAAAAAAAAAAAAAAAA 1766

RESULT 13
US-08-245-295-4
Sequence 4, Application US/08245295
Patent No. 5700658
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Kilgannon, Patrick D.
TITLE OF INVENTION: ICAM-4 Materials and Methods
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
ADDRESSER: 233 South Wacker Drive, Suite 6300
STREET: Street
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/245,295
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061

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FILING DATE: 05-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 27866/32055
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1781 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 16..1659
US-08-245-295-4

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Query Match 3.2%; Score 37.2; DB 1; Length 1781;
Best Local Similarity 63.3%; Pred. No. 0.4;
Matches 57; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

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Oy 1063 aaggatgctgcgtcgaagtcacagctggttaataacttatgtcta 1122
Db 1677 AAGTTGGGGGGGGCTTGCTGTGCTCCAGATTCCGACCATTAAGCTTCAAACTCC 1736
Oy 1123 ctgtcaaaaaaaaaaaaaaaaaa 1152
Db 1737 CAAAAAAAAAAAAAAAAAAAAA 1766

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RESULT 14
US-08-481-130-4
Sequence 4, Application US/08481130
Patent No. 5702917
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Kilgannon, Patrick D.
TITLE OF INVENTION: ICAM-4 Materials and Methods
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,130
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:

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APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAMS, JR. JOSEPH A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32713
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1781 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 16..1659
US-08-481-130-4

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Query Match 3.2%; Score 37.2; DB 1; Length 1781;
Best Local Similarity 63.3%; Pred. No. 0.4;
Matches 57; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

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Oy 1063 aaggatgctgcgtcgaagtcacagctggttaataacttatgtcta 1122
Db 1677 AAGTTGGGGGGGGCTTGCTGTGCTCCAGATTCCGACCATTAAGCTTCAAACTCC 1736
Oy 1123 ctgtcaaaaaaaaaaaaaaaaaa 1152
Db 1737 CAAAAAAAAAAAAAAAAAAAAA 1766

```

```

RESULT 15
US-08-656-984A-4
Sequence 4, Application US/08656984A
Patent No. 5753502
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Kilgannon, Patrick D.
TITLE OF INVENTION: ICAM-4 Materials and Methods
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/656,984A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992

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1      PRIOR APPLICATION DATA:
2      APPLICATION NUMBER:  US 07/889,724
3      FILING DATE:  26-MAY-1992
4      PRIOR APPLICATION DATA:
5      APPLICATION NUMBER:  US 07/894,061
6      FILING DATE:  05-JUN-1992
7      PRIOR APPLICATION DATA:
8      APPLICATION NUMBER:  US 08/009,266
9      FILING DATE:  22-JAN-1993
10     PRIOR APPLICATION DATA:
11     APPLICATION NUMBER:  US 08/102,852
12     FILING DATE:  05-AUG-1993
13     PRIOR APPLICATION DATA:
14     APPLICATION NUMBER:  US 08/245,295
15     FILING DATE:  18-MAY-1994
16     PRIOR APPLICATION DATA:
17     APPLICATION NUMBER:  US 08/485,604
18     FILING DATE:  07-JUN-1995
19     ATTORNEY/AGENT INFORMATION:
20     NAME:  WILLIAMS, DR. JOSEPH A.
21     REGISTRATION NUMBER:  38,659
22     REFERENCE/DOCKET NUMBER:  27866/33321
23     TELECOMMUNICATION INFORMATION:
24     TELEPHONE:  312-474-6300
25     TELEFAX:  312-474-0448
26     TELEX:  25-3856
27     INFORMATION FOR SEQ ID NO:  4:
28     SEQUENCE CHARACTERISTICS:
29     LENGTH:  1781 base pairs
30     TYPE:  nucleic acid
31     STRANDEDNESS:  single
32     TOPOLOGY:  linear
33     MOLECULE TYPE:  CDNA
34     FEATURE:
35     NAME/KEY:  CDS
36     LOCATION:  16..1659
37     US-08-656-9844-4

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Query Match Similarity 3.28; Score 37.2; DB 1, Length 1781;
Best Local Similarity 63.38; Pred. No. 0.4;
Matches 57; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

OY 1063 aaggagagcagtcgtaagagagactcaagacgtgttaataactatgcca 1122
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Db 1677 AAGGTGGCGGGGGCTGGCTGTCCTCAATTCCTCCACACATAAGCCTCAAACTCC 1736
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OY 1123 ctgtcaaaaaaaaaaaaaaaaaa 1152
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Db 1737 CAAAAAATAAAAAAAAAAAAAAAAAA 1766

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